

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2003, 12:27:54 ; Search time 732 Seconds
(without alignments)
4844.670 Million cell updates/sec

Title: US-10-082-894-1

Perfect score: 1719

Sequence: 1 gtttaattaccaaaatgttga.....aaatctccgttataaaaatt 1719

Scoring table: IDENTITY_NUC
Gapop 10.0 , gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
 1: /cgn2_6/podata/1/pubpna/us07_pubcomb.seq:
 2: /cgn2_6/podata/1/pubpna/us06_new_pub.seq:
 3: /cgn2_6/podata/1/pubpna/us06_new_pub.seq:
 4: /cgn2_6/podata/1/pubpna/us06_pubcomb.seq:
 5: /cgn2_6/podata/1/pubpna/us07_new_pub.seq:
 6: /cgn2_6/podata/1/pubpna/pc0tus_pubcomb.seq:
 7: /cgn2_6/podata/1/pubpna/us08_new_pub.seq:
 8: /cgn2_6/podata/1/pubpna/us09_pubcomb.seq:
 9: /cgn2_6/podata/1/pubpna/us09a_pubcomb.seq:
 10: /cgn2_6/podata/1/pubpna/us09b_pubcomb.seq:
 11: /cgn2_6/podata/1/pubpna/us09c_pubcomb.seq:
 12: /cgn2_6/podata/1/pubpna/us09_new_pub.seq:
 13: /cgn2_6/podata/1/pubpna/us10a_pubcomb.seq:
 14: /cgn2_6/podata/1/pubpna/us10b_pubcomb.seq:
 15: /cgn2_6/podata/1/pubpna/us10_new_pub.seq:
 16: /cgn2_6/podata/1/pubpna/us60_new_pub.seq:
 17: /cgn2_6/podata/1/pubpna/us60_pubcomb.seq:
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Sequence 8836, App
Sequence 152, App
Sequence 1425, App
Sequence 1425, App
Sequence 1425, App
Sequence 1425, App
Sequence 1, Appli
Sequence 23424, A
Sequence 6690, App
Sequence 200181, App
Sequence 138, App
Sequence 475, App
Sequence 8257, App
Sequence 63, Appli
Sequence 4, Appli
Sequence 2144, App
Sequence 519, App
Sequence 543, App
Sequence 5075, App
Sequence 28, Appli
Sequence 42, Appli
Sequence 31828, A
Sequence 11, Appli
Sequence 42, Appli
Sequence 4050, App
Sequence 4173, App
Sequence 325, App
Sequence 128, App
Sequence 4012, App

ALIGNMENTS

RESULT 1
US-08-781-986A-128
; Sequence 128, Application US/08781986A
; Publication No. US2003054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08781,986A
; FILING DATE:

CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 128:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6048 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

Result No.	Score	Query Match	Length	DB ID	Description
1	261.4	15.2	6048	8	US-08-781-986A-128
2	222.2	12.9	1620	10	US-09-895-913A-105
3	175.6	10.2	1041	10	US-09-974-300-696
4	161.2	9.4	881	10	US-09-974-300-5220
5	84	4.9	1728	10	US-09-938-842A-2675
c 6	81.4	4.7	484	9	US-09-159-463-34
c 7	81.4	4.7	484	9	US-09-738-043-34
c 8	69.4	4.0	400	8	US-08-781-986A-782
c 9	51.8	3.0	264	10	US-09-974-300-894
c 10	42.6	2.5	279	9	US-09-294-093B-4249
c 11	42.4	2.5	2000	10	US-09-938-842A-2831
c 12	40	2.3	640681	10	US-09-790-988-1
c 13	39.8	2.3	2861	9	US-09-887-586A-55
c 14	39.8	2.3	2861	11	US-09-903-012-55
c 15	39.8	2.3	2861	13	US-10-041-007-3
c 16	39.8	2.3	2861	13	US-10-041-007-3

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

; TOPOLOGY: linear
; US-08-781-986A-128

316	GCCPTCAAACGATTAATTAAAACAACCCGGCTTTTTT	- - - - - AAACRCGATCCAA	368
347	AGAAGGGACTGGTGGATTCGATTATTAGGACTGTTAGCGATGGTGTGTCACCTCTC	406	
369	AAAACCCCSTGG- - - TGCATCTTATGGGTTTAAATGAGGATGSGAGGCTGCGATC	423	
407	ATATGATCATCTTGTGGCTGATACGTGATTAACACATACTAGTGCCTAACAGTGGT	466	
424	ACATGAGGATTTCGCTCTGGTTAGGTGTTAAATCCCA - - TAAAGAACTCT	480	
467	TCACTCACATTTCGCTGATGGTGGAGATACTTCGCCAACAGTGGAGCTGGTTATCTTG	526	
481	GTCCTACATTAACTACCGATGGGGATGTCGCTCTAAAGCGCTTAACTTAACTTAA	540	
527	AACACTCTCTCAATTATATGCTTGGAAAAGTAGCGAGAATTGGTACTATTACCTGGAC	586	
541	AACATATG - - - AACATATCTGCAATGAAACGATTCAATCGTACCCATAGGGCTG	594	
587	GTTATTGCAATGGTAGGGACAAAGATGGGGTAAAGATGGCTTGTAGGCAA	646	
595	GTTTTATGCCATTGGATAGGGATAACGCCCTGGTGAAGGATGGCTGGTGTCA	649	
647	TTGGTGGAGGTTATGGACAAAGGCCACCGCTGTGATAGGGCTGGTGTAGAGGCG	706	
650	- - - TAGCTTAATGGGCTTAATCACAGCCTTAAAGGCCCTTAGGGACTATACTCAAAAGCC	705	
707	GATATGCTCAATCTGAGACTGAGGAATTTCGAAACCAATGGTTTGGAGATGGC	766	
706	AGTACGATTAATATCACCGATGAGTTTACATGCCGCTGTGTTAAATTATTCG	765	
767	GAGTAAAGATGACGACTCTTATTCGTCAAATTATCGCTGATCGTATGCGTCA	826	
766	GCATGCCAAGTGTAGAGGTTTATTTCAATTTCAGGAGTAAAGGGTAGACAAA	825	
827	TTTGSGAATTTGGTCTCGAAACGTTATAAGCTTAAAGCTTAAAGCTTAAAGCT	896	
826	TGTTGAGGCGTTTAAGCCAAAACATTCACTGGCCTTAAGGCCCAAGTT - - - TTAA	879	
887	AAAATATTGAGATTAGGGATGACCAATCAATAAAAGGTTCCATTTCCATGTTAT	946	
880	AAAATCTCCATATCGTACCATGAGCCCTTACACTTCCCTACCCCTTACCTGTTAT	939	
947	TCCCCACCTGTGACTCTACATGCTGCTTACCTCTCATGTTACCTCTCTCAAGGAGTTACTC	100	
940	TCCCCAAAGAAAGGGTCAAAACACCTCGCTGAACTGAAAAAATACGGCATGTCACACACATGACCC	999	
1007	ATTTCACATGCGGAACCTGAAACTATCTCTCATGTTACCTCTCATGTTACCTCTCTCAAGGAGTTACTC	106	
1000	AAAGCCATATCGCTGAACTGAAACGAAACCTCGCTGAACTGAAACCTTTCATGCGGAG	105	
1067	GAGAAGTCAATTCCAAGATGAAAGCGCTTGTGATGGTCCGTCACCCAAAAGAGTTGCTA	112	
1060	TGGAAACGCCCTTTAAATGAAACGGGTGCTTATCCAAGCCCTA - - - TAGTTACCA	111	
1127	CATATGATTTAAACCGAAATGATGCTGCTGGAATTGGCGAAAAAAATGGTCGAGCAA	118	
1117	CTTAGACTTAAAGCTGTAAGGCTTAAGGCTAAAGAAGTAACCCCTTGGGTGTTAGGC	117	
1187	TTGAGTCAGGAGGATGCCCTGGTATGTCGAATTGGCTCTGCTGAGCTGGATTTGGAC	124	
1177	TGAANACTAGGACGGA - - - TTGATCATTTGGAATTTGGCATATGGTAGGGC	123	
1247	ATACTGTTAAATTGACACCTGCGTCAAAGGATGTCAGTGCAGGGCAATTGGAA	130	
1234	ATACCGGAAATTGAGCGATCCAAACTTAAATTAGTGTCTTATGGTACTTCGATCTGAA	129	
1307	AGATTTGAGGACTCCAAACTTAAATTAGTGTCTTATGGTACTTCGATCTGAA	136	
1294	AAATCTCTTCACTGGCTTAAACAAATGGATTACGCCATGCTTTAACCGGATCTGGA	135	
1367	ATGCGAGAAGATGAACTTGTAGCGAGCTTAAAGCGGTGAGCAGTGTGGG	1381	

Db	1354	ATTGGCAGGCCATGTA	1368
	RESULT	3	
	US-09-974-300-696		
	; Sequence 696; Application US/099		
	; Patent No. US200214672A1		
	; GENERAL INFORMATION:		
	; APPLICANT: Berka, Randy M.		
	; ATTENDEE: Clausen, Ib Groth		
	; TITLE OF INVENTION: Methods For		
	; TITLE OF INVENTION: Expression		
	; FILE REFERENCE: 10085 500-US		
	; CURRENT APPLICATION NUMBER: US/		
	; CURRENT FILING DATE: 2001-10-01		
	; PRIOR APPLICATION NUMBER: 09/681		
	; PRIOR FILING DATE: 2000-10-06		
	; PRIOR APPLICATION NUMBER: 60/271		
	; PRIOR FILING DATE: 2001-03-27		
	; NUMBER OF SEQ ID NOS: 8481		
	; SOFTWARE: FastSEQ for Windows V		
	; SEQ ID NO: 696		
	; LENGTH: 1041		
	; TYPE: DNA		
	; ORGANISM: bacillus licheniformis		
	US-09-974-300-696		
	Query Match	10.2%	:
	Best Local Similarity	53.0%	:
	Matches	460	Conservative
			0
Qy	583	GACCGTTATTATGCAATGGAA	
Db	57	GGCCATGCACTATCAAATGGAA	
Qy	643	GCATCTGTGGAGGTATTGG	
Db	117	GCCATGGCATGGAGGAGGG	
Qy	703	GAGGATATGGCAATCTGA	
Db	171	GTATCTTATGAAACGGATT	
Qy	762	-----TGCGCG	
Db	231	AACGGGAACCTGTGGCAC	
Qy	808	GCTGATCGTATCGTCATAAT	
Db	291	CCCGACCGTGGATCCCGAT	
Qy	868	AGTTGGTCTCTCACCTAA	
Db	351	CGGGGACAAGCATCGAA	
Qy	928	TTTCCATTTCATCGTTAT	
Db	411	GTTGACGGATACGGGCAATT	
Qy	988	GCTTCAGGAGTTACTCA	
Db	471	TCCCCAACGGCTGAAAGCA	
Qy	1048	TTCTTCTTAAATGGGTCTCG	
Db	531	TCTTATGAGGGGAGCG	
Qy	1108	TACCAAAAGAATGGTGTAC	
Db	591	TGGCTTA---AAGTCGAAAC	
Qy	1168	AAAAAAATGGTGGAGCAAT	

648	GATGCGCTGTCAAGAAATTGAGCTGAAAAGATAAGGGATCATCCTCAACTTGGCC	707
1228	CCTCCGTACATGGGACATACTGGCTAAATTGGAAACCTGCCGTCAAAGCATGTCAGCT	128
708	AACCTGTACATGGTGGACATTCAAGGAAAGTCAGGCTAACGCAAGCTAACGGCG	767
1288	ACTGAGGGAATTTGGAGAATTTGGAGCATGCCAAACTTATAATTAGCTCTPATG	134
768	GTTGAGGAGTCGGCTGGCGAAGTGTGATGCAATTCTTGCAAAAGGGCTACGGATT	827
1348	GTTACPTCGATCATGAAATTGCTGAGAAATGGCTCCGATGGTAGTGAACATCT	140
828	ATTACGGCCACCGGTACCGTAGCGAGCTGCTGTTACCGGAAAGCCGACACC	887
1408	GCACATACCTGCAATTGGTCCCCATTAA	1435
888	GCACATACGACAACCGGTTCCGTCA	915
RESULT 4		
-09-974-300-5220		
Sequence 5220, Application US/09974300		
Patent No. US2002146721A1		
GENERAL INFORMATION:		
APPLICANT: Berka, Randy M.		
APPLICANT: Clausen, Ib Groth		
TITLE OF INVENTION: Methods For Monitoring Multiple Gene		
FILE REFERENCE: 10085_500-US		
COURRENT APPLICATION NUMBER: US/09/974,300		
CURRENT FILING DATE: 2001-10-05		
PRIOR APPLICATION NUMBER: 09/680,598		
PRIOR FILING DATE: 2000-10-06		
PRIOR APPLICATION NUMBER: 60/279,526		
PRIOR FILING DATE: 2001-03-27		
NUMBER OF SEQ ID NOS: 8481		
SOFTWARE: FastSEQ for Windows Version 4.0		
SEQ ID NO 5220		
LENGTH: 881		
TYPE: DNA		
ORGANISM: Bacillus clausii		
-09-974-300-5220		
Query Match	9.4%	
Best Local Similarity	52.7%	
Matches	436;	
Conservative	0;	
Mismatches	368;	
Indels	24;	
Gaps	3	
561 CGGAGAAATTGGCTRACTATTACTGGACGTTATTATGCAATGGCAAAAGATGGAA	620	
50 CGGTAACTGGGACTGTGCAAGCCGTTACTATGCAATGGTCGCAAAAGCTGGAA	109	
621 GCGTATTAAATGGTTATGGGAATGGTGGGATTTGGCAAAAGGCCGTTGGAA	680	
110 TCGAATGTGAAAAGTCATACCGTGGAAATGGTTATGGCAGGGCC-----CTNGCCTATAA	163	
681 TAAGGGCTGTGATGGTTAGAGGGATATGCTCAATCTGAGACTGCAATTCTGAA	740	
164 GRACGGCTTAGGGCTGCTGAGAGCTACAAAACACATGTTGACGAGTTGTCT	223	
741 ACCAATGGTTTTGGGAGATGGCGA-----GTAAGATGCAATAC	785	
224 TCCGTCGCTGTTATCACAGAGATGGTACACCTGTAGCAACTGTCAGAACGATGCG	283	
786 TCTTATTCTCTCAATTATCTGTCGATGGCTATGCGTAAATTGTAATGTTGGCT	845	
284 CGTCATTCTGCAATTCTGCGCTGACCGTGTATCCAGCTACACAGTTTCAGCAA	343	
846 CGAACGGTTAAAGATCTTAATTACTTCGGTTCTCACCCTAAATATTAGATAGTGG	905	
344 TGAACACTTCTGGGTGACCCAGGGAAAAGATGCGAAACGCCCTCCATTGTCGTC	403	
906 GATGACCCCAATACATAAAGAGTTCCCATTCATCGTATTCCACCTGACTAC	965	

Qy 1183 CAAATGAGTAGCAGGCAGGCAATTCTTGGTTAGTCATTGGCATCTGCGCTCTGACATGGT 1242
 Db 1288 GGAACTCTTAGGCAAGTGTGATCAGTGGCAAGTAAACATGGAGATATGGT 1347

Qy 1243 GGACACTACTGTAATTGAACTGGCATGGTCAAAGCATGTCAGCTACTGAGGGCAATT 1302
 Db 1348 GTCATACAGGGATAATGAACCACGGTGTGCAAGTGGCAACTGGTACATGGTGTG 1407

Qy 1303 GGAAGAATATGGCATGGCAAACTATAATTACGTTCTPATGGTTACTCCGATCAT 1362
 Db 1408 AGATGATTGATGCAATGCGAACAGTGAAGGAATTATGTTGACTGTGATCAC 1467

Qy 1363 GAAATGCTGAGAAGATGAT 1382
 Db 1468 GAAAACCGCAGGACATGGT 1487

RESULT 6
 US-09-159-469-34/C
 Sequence 34, Application US/09159469
 Patent No. US20020064535A1
 GENERAL INFORMATION:
 / APPLICANT: Reed, Steven G.
 / ATTORNEY/AGENT INFORMATION:
 / APPLICANT: Houghton, Raymond J.
 / TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND THERAPY OF EHRLICHIA INFECTION
 NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:
 ADDRESSEE: SPEED and BERRY, LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/159,469
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/106, 582
 FILING DATE: 29-JUN-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE DOCKET NUMBER: 210121.439C2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-622-4900
 TELEFAX: 206-682-6331
 INFORMATION FOR SEQ ID NO: 34 :
 SEQUENCE CHARACTERISTICS:
 LENGTH: 484 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 / ORGANISM: Ehrlichia
 us-09-159-469-34

Query Match Score 4.7%; Length 484;
 Best Local Similarity 53.4%; Pred. No. 5.2e-10;
 Matches 244; Conservative 0; Mismatches 201; Indels 12; Gaps 3;

Qy 245 CTGGAGAGTTATGGACAGGGCTTAATGGAAATTCTGAGTTGGACATTGGAAATTGGAT 273
 Db 386 GCGGCAGGATGCTTCAGTCAGTGGAAATCAGAGTGGCAACATAAGTATGGAT 364

Qy 305 TTGTTCACAATCCCTGAGATTGTCAGTCAGGGTCAAGAGGGGAGTGGTCGAT 364
 Db 332 TTCAAGAAGATCCTAATTGGACATTGGCAATATAGGGAAAGGGTGGGGTAT 273

Qy 305 TTGTTCACAATCCCTGAGATTGTCAGTCAGGGTCAAGAGGGGAGTGGTCGAT 364
 Db 332 TTCAAGAAGATCCTAATTGGACATTGGCAATATAGGGAAAGGGTGGGGTAT 273

Qy 365 TGCATTTAGGACTGCTTCACTCTCATATTGATCATCTTTGCTG 424
 Db 272 GCGCACATGATGGTCGCTTCAGTGGCAAGTGGCACTCTCATGGCAACATGGAAA 213

Qy 365 TGCATTTAGGACTGCTTCACTCTCATATTGATCATCTTTGCTG 424
 Db 272 GCGCACATGATGGTCGCTTCAGTGGCAAGTGGCACTCTCATGGCAACATGGAAA 213

Qy 425 CGTTGATACGCTGCAATTAAACAAATTACAGTGGCAAGGGTTTCACTCATCTTTGCTG 484
 Db 212 CCATTAT--TGAGGTATCACGGATTGGCATCAGGTTTAACTGATCTAATCTAG 156

Qy 485 ATGGTCGAGATACTCTGCCCACAAAGTGGCTGTTATCTGAAACACTCTCAATTAA 544
 Db 155 ATGGTAGGGATGTT - -CCACCGCTCTGTTGAGAGTATATGGTATGCTGAAGCTA 99

Qy 545 TTGCCTGGAAAAGTACGGAGAAATTGGCTACTATTACTGGAGCTTATTATGCAATGGATA 604
 Db 98 AAATGGACACTTAATGCCGAAATTGCTACTGGCTTACATGCTATGGAT 39

Qy 605 GGAAAAAATGGGGCGTATTAAAGTGGCTTATA 641
 Db 38 GGGATAATCGCCTGSGTATGGACATGTAAGCTTGA 2

RESULT 7
 US-09-798-042-34/C
 Sequence 34, Application US/09798042
 ; Patent No. US2002006843A1
 GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; ATTORNEY/AGENT INFORMATION:
 / APPLICANT: Lodes, Michael J.
 / APPLICANT: Houghton, Raymond L.
 / APPLICANT: McNeil, Patricia D.
 / TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF EHRLICHIA INFECTION
 / FILE REFERENCE: 210121.439C7
 / CURRENT APPLICATION NUMBER: US/09/798, 042
 / CURRENT FILING DATE: 2001-03-02
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 34
 ; LENGTH: 484
 ; TYPE: DNA
 ; ORGANISM: Ehrlichia sp.
 US-09-798-042-34

Query Match Score 4.7%; Length 484;
 Best Local Similarity 53.4%; Pred. No. 5.2e-10;
 Matches 244; Conservative 0; Mismatches 201; Indels 12; Gaps 3;

Qy 185 ATGTTGATGGCAGAGGCTTAATGGAAATTCTGAGTTGGACATTGGAAATTGGAG 244
 Db 446 ATGTCGGATGCTTCAGGTCAGTGGGAATTCAAGATGGCACTATGGAT 387

Qy 245 CTGGAGAGTTATTCAGTCAGTGGCAATTAAATTGGCTGAAATTGGCTGAACTGGAT 304
 Db 386 GCGGCAGGATGCTTCAGTCAGTGGCAACTGGATCTGGCAATTGGAT 333

Qy 305 TTGTTCACAATCCCTGAGATTGTCAGTCAGGGTCAAGAGGGGAGTGGTCGAT 364
 Db 332 TTCAAGAAGATCCTAATTGGACATTGGCAATATAGGGAAAGGGTGGGGTAT 273

Qy 365 TGCATTTAGGACTGCTTCACTCTCATATTGATCATCTTTGCTG 424
 Db 272 GCGCACATGATGGTCGCTTCAGTGGCAAGTGGCACTCTCATGGCAACATGGAAA 213

Qy 425 CGTTGATACGCTGCAATTAAACAAATTACAGTGGCAAGAGGGGAGTGGTCGAT 364

Db 212 CCATATT--TGAGTTATCACCGGATTGGCATCAAGTTTATACATGTAATTCTAG 156
 Qy 485 ATGGCAGATACTTCGCCAACAGTGGACTGGTTATCTGAAACTCTCAATT 544
 Db 155 ATGGTAGGGATTT--CCACCGCGTCTGCTGAAGTATCGGTATGCTGAACGCTA 99
 Qy 545 TTGCTTGGAAAAGTACGGAAATGCTGACTATTACGTGAACTTATGCAATGGATA 604
 Db 98 AAATGGGACTTAAATGCCGAATTGCTACTGTGAGGGTTACTATGCTATGGATA 39
 Qy 605 GGGACAAAAGATGGGAGCTTAAATGCCGAATTGCTACTGTGAGGGTTATGAA 641
 Db 38 GGATATACTGCCTGTAGACATGAACTGTAAGCTTATGAA 2

RESULT 8

US-08-781-986A-782

Sequence 782, Application US/08781986A

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5255

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MS DOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/781,986A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; ATTORNEY/AGENT INFORMATION:

; NAME: Benson, Bob

; REGISTRATION NUMBER: 30,146

; REFERENCE/DOCKET NUMBER: PB248PP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 309-8504

; TELEFAX: (301) 309-8512

; INFORMATION FOR SEQ ID NO: 782:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 400 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; US-08-781-986A-782

Query Match

Best Local Similarity 49.9%

Matches 195; Conservative 0;

; Mismatches 195; Indels 1; Gaps 1;

; Score 69.4; DB 8; Length 400;

; Pred. No. 4.3e-07;

; Result 10

Db 2 TGAATATCGGTGAGGAGCTTACGTTATCAAAGTTAATCAATTCTAG 61

Qy 293 AACCAAAGAGTGTGTTACAATCCTCATGTTGCACTGGCTGCAAGAGG 352

Db 62 AAGACGGGAGATTCCTGAAATGATGTTAAATGCAATGCACTGTAATC 121

Qy 353 GGAGTGGTCGATTCGCAATTAGGACTGGTATGGATGTTGCTCACTCTCATATTG 412

Db 122 ATGATTCACTCGTGTACACATCTGGTATGGTGTACAGTCATACAGTCATA 181

Db 213 ATCATCTTGGCTGTGATACTGTCATTAAGCAATTACAAGTCCAAAGGTTCATTTC 472
 Qy 182 AACATTATTGCTTGTGAACTGTGTTAAACAAAGNGTGAATGTTACGTAC 241
 Db 473 ACTTTTTGCTGATGTTGCTGAGATACTTCGCCAACAAAGTGGCTGGTTATCTGAACAC 532
 Db 242 ACCGATTTAGTGGCCCTGA-CGTAGATCAAATCGCTTGAAATACATGAAAGAG 300
 Qy 533 TTCTCAATTATGCTGGAAAGTCCGGAAATGGCTACTATTAGTGGCTTATT 592
 Db 301 ACTGAAGCTAAATCCATGAATNAGGCATNGGCCATTGACCGGGCTGGCGTAATA 360
 Qy 593 ATGCAATGGTAGGGACAAAAGATGGGGCG 523
 Db 361 AGCCCAANGGACCGGGCRAACCGTTGGACCG 391

RESULT 9

US-09-94-300-894/c

Sequence 894, Application US/09974300

; Patent No. US20020146721A1

; GENERAL INFORMATION:

; APPLICANT: Berk, Randy M.

; CLAUSEN, Ib Groth

; TITLE OF INVENTION: Methods For Monitoring Multiple Gene

; Expression

; FILE REFERENCE: 10085_500-US

; CURRENT APPLICATION NUMBER: US/09/974,300

; PRIORITY NUMBER: 09/680,598

; PRIORITY FILING DATE: 2001-10-06

; PRIORITY NUMBER: 60/279,526

; PRIORITY FILING DATE: 2001-03-27

; NUMBER OF SEQ ID NOS: 881

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 894

; LENGTH: 264

; TYPE: DNA

; ORGANISM: Bacillus licheniformis

; US/09-974-300-894

Query Match

Best Local Similarity 54.5%

; Matches 126; Conservative 0;

; Mismatches 102; Indels 3; Gaps 1;

; Score 51.8; DB 10; Length 264;

; Pred. No. 0.0074;

; Result 10

Db 65 TTATGATGGATGGCCCTTCGGATGAAACAGCGGAATGCTAAAGCTAAAA 124

Db 261 TTATGATGGTTGGACTAAGGCACGAAACCCCTCGGAAACCGCCTGGAA 202

Qy 125 CGCTTATTATGGAAAACCTTGTCTGAAATTGG -- CAAANATTGAAAGCAGCGTC 181

Db 201 AACCGAATTGACCTTGACCGTTACGTCGACCAGACGCTGACAGCTTCAG 82

Qy 182 TTATGTTGGATGCCAACAGGTTAAATGGAAATTCCTGAAGTGGGATATGG 142

Db 141 AACGGTGGAGGCTCCAGCGCAGATCGGAACTCGAACGGCCATCGATA 82

Db 242 GGCTGGAAAGAGTTATTTATCAAGATATTGTTGGAATTATTGGCTGTTTC 292

; Sequence 4299, Application US/09294093B

; Patent No. US20100133541

; GENERAL INFORMATION:

; APPLICANT: LaJudi, Raghunath, V.

; ATTORNEY: Ito, Laura, Y.

; SOFTWARE: Sherman, Bradley, K.

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL

; FILE REFERENCE: PL-0009 US

CURRENT APPLICATION NUMBER: US/09/294,093B
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/092,567
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO: 4299
; LENGTH: 279
; TYPE: DNA
; ORGANISM: sea mays
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO. US20010051335A1 700353690H1
; US-09-294-093B-4299

Query Match 2.5%; Score 42.6; DB 9; Length 279;
Best Local Similarity 51.3%; Pred. No. 1.4;
Matches 99; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy 1120 GTTGCTACATATGATTAAACCAGAATGATGCTGGAGTGTGCTGGAAAATGGTC 1179
Db 20 GGTATACATCAATGGTGCACCCAGATGAAGGCCCTCAAACTGCTGAAAGCTAGG 79
Qy 1180 GAGCAAATTGACTCAGCGAGGATCCTTGGTTATGCAATTTCGCCCTCGACATG 1239
Db 80 GACGCTCTCTTAAGTGGAAAGTTGACCGTAGTGTCAACCTGCCAAATGGACATG 139

Qy 1240 GTGGCATACATGGTAAATTGAACTGGCCCTCAAGGCATGCAACTACTGACGGGCA 1299
Db 140 GTGGTACACTGGGATATTGAGGCCACCGTTGTTGCTTCAAGCGCTGATGAGCT 199

Qy 1300 ATTGGAAAGATAT 1312
Db 200 GTTAAGATCATCT 212

RESULT 11
; Sequence 2831, Application US/09938842A
; Patent No. US2002160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, JoeL
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SRIPL300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO: 2831
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-938-842A-2831

Query Match 2.5%; Score 42.4; DB 10; Length 2000;
Best Local Similarity 60.3%; Pred. No. 4.6;
Matches 70; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 1587 TGAACAGAGGATAAGAAGTTAATGACAATAGGAAATAATATGAGCTGCTATACAA 1646
Db 186 TAACATTAAGATAATTAGTAAACAGATAATTGATATACTTATGCRCCCATATA 127
Qy 1647 GCAATTTAAATTTAGTAAACAGATAATTGATATACTTATGCRCCCATATA 1702

Db 126 GTATAATTAAATTTATAATTACTAATATATAATATCATATGAA 71
; RESULT 12
; Sequence 1, Application US/09790988
; Patent No. US200212768A1
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, Shuji
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIOKU
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,938
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
; US-09-790-938-1

Query Match 2.3%; Score 40; DB 10; Length 640681;
Best Local Similarity 59.8%; Pred. No. 4e+02;
Matches 67; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy 1077 ATTCAGATGAGAGCGGTGATGGTTCCGTCACCAAAAGAAGTGTCTACATATGATT 1136
Db 467290 ATTAAAAAAATAGAACGATGTTTATGATGTTCTTATGAAAGATAAGATAAGTT 467231
Qy 1137 AAACCAAAATGAATGCTGGTGGCCAAAATATGGTCGAGCAATT 1188
Db 467230 AATTCAGAAATGGCATCTTATTACTAGAAAAAAATGTATGChGAAT 467179

RESULT 13
; Sequence 55, Application US/09887586A
; Patent No. US2002094556A1
; GENERAL INFORMATION:
; APPLICANT: CHAPPELL, Joseph P.
; APPLICANT: STARKS, Courtney M.
; APPLICANT: MANNA, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1998-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 55
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(2606)
; OTHER INFORMATION: abietadiene synthase
; US-09-887-586A-55

Query Match 2.3%; Score 39.8; DB 9; Length 2861;
Best Local Similarity 53.5%; Pred. No. 25;
Matches 83; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Qy 1449 AACATTGTTAAATCGACTCCACCTACTGGAGATGATGCCAAGAACGTGACGAGC 1508
 Db 2177 AACAGTCGTCATAGTGCTCTTCACTGGGGTTCTAACAGTAAGTGAAGTCTC 2236
 Qy 1509 CTTACGTGATGTTGCAACGGACTGTCTCAATTAAATGGCTTACCTGTACCGCCGGAGAT 1568
 Db 2237 CAAAATGATGCGAACTTAGATTCTAACICATGGCTTAACAGGCCTGGTGGTGA 2296
 Qy 1569 GGATGGGTTCCCTTACTGTAAACGAGGGATAAG 1603
 Db 2297 TGACACCAAAACTTATCAGGCAGAGGTCAAG 2331

RESULT 14

US-09-903-012-55

; Sequence 55, Application US/09903012

; Patent No. US20020094557A1

; GENERAL INFORMATION:

; APPLICANT: Chappell, Joseph P.

; NO. US20020094557A1, Joseph P.

; APPLICANT: Starks, Courtney M.

; NAME/KEY: Manna, Kathleen R.

; TITLE OF INVENTION: SYNTHASES

; FILE REFERENCE: 07678-025001

; CURRENT APPLICATION NUMBER: US/09/903, 012

; CURRENT FILING DATE: 2001-07-11

; PRIOR APPLICATION NUMBER: 09/398, 395

; PRIOR FILING DATE: 1999-09-17

; PRIOR APPLICATION NUMBER: 60/100, 393

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: 60/130, 628

; PRIOR FILING DATE: 1999-04-22

; PRIOR APPLICATION NUMBER: 60/150, 262

; PRIOR FILING DATE: 1999-08-23

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO: 55

; LENGTH: 2861

; TYPE: DNA

; ORGANISM: Abies grandis

; FEATURE: CDS

; LOCATION: (3) ..(2606)

; OTHER INFORMATION: abietadiene synthase

US-09-903-012-55

Query Match Score 2.3%; DB 11; Length 2861;

Best Local Similarity 53.5%; Pred. No. 25; Matches 83; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

Qy 1449 AACATTGTTAAATCGACTCCACCTACTGGAGATGATGCCAAGAACGTGACGAGC 1508

Db 2177 AACAGTCGTCATAGTGCTCTTCACTGGGGTTCTAACAGTAAGTGAAGTCTC 2236

Qy 1509 CTTACGTGATGTTGCAACGGACTGTCTCAATTAAATGGCTTACCTGTACCGCCGGAGAT 1568

Db 2237 CAAAATGATGCGAACTTAGATTCTAACICATGGCTTAACAGGCCTGGTGGTGA 2296

Qy 1569 GGATGGGTTCCCTTACTGTAAACGAGGGATAAG 1603

Db 2297 TGACACCAAAACTTATCAGGCAGAGGGTCAG 2331

Search completed: August 4, 2003, 15:35:16
 Job time : 736 secs

RESULT 15

US-09-900-797-55

; Sequence 55, Application US/09900797

; Publication No. US20030087406A1

; GENERAL INFORMATION:

; APPLICANT: Chappell, Joseph P.

; APPLICANT: No. US20030087406A1, Joseph P.

; APPLICANT: Starks, Courtney M.

; APPLICANT: Manna, Kathleen R.